REMARKS

Reconsideration and withdrawal of the rejections of this application and consideration and entry of this paper are respectfully requested in view of the herein remarks, which place the application in condition for allowance.

1.   Status Of Claims And Formal Matters

Claims 1-8, 10-14 and 16-33 are under consideration in this application. Claim 1 has been amended. No new matter has been added by this amendment.

Support for the recitation that the truncated Mtu *recA* intein is ΔI-CM or ΔI-SM is found on page 12, line 28, page 13, line 1, page 17, line 29, page 24, lines 5-9, page 26, lines 28-30, page 36, lines 7-9 and 23-26 and Figure 2 of the specification as originally filed. Support for a full-length Mtu *recA* intein having a V67L and/or a D422G mutation(s) is found on page 24, lines 10-30 and page 26, lines 28-30 of the specification as originally filed.

Applicants thank the Examiner for withdrawing the objection of claim 11-33 for being improper multiple dependent claims.

It is submitted that the claims, herewith and as originally presented, are patentably distinct over the prior art cited by the Examiner, and that these claims were in full compliance with the requirements of 35 U.S.C. § 112. The amendments of the claims, as presented herein, are not made for purposes of patentability within the meaning of 35 U.S.C. §§§§ 101, 102, 103 or 112. Rather, these amendments and additions are made simply for clarification and to round out the scope of protection to which Applicants are entitled.

2.   The Rejections Under 35 U.S.C. § 112, First Paragraph, Are Overcome

Claims 1-8, 10, 11-14 and 16-33 were rejected under 35 U.S.C. § 112, first paragraph, as allegedly containing failing to comply with the written description requirement. This rejection is respectfully traversed. This rejection is moot in light of the amendments to the claims submitted herein.

The Examiner alleges that the claims encompass truncated Mtu inteins with the endonuclease domain deleted, and V67L and/or D422G mutations or any intein having a D to G mutation in a location corresponding to residue 422 of the full-length Mtu intein, or any mutein using the homology limitation which is "very similar" to the muteins recited above. The

Examiner further contends that the specification and claims do not indicate what distinguishing attributes are shared by the members of the genus and thus, the scope of the claims include numerous structural variants, and the genus is highly variant because a significant number of structural differences between genus members is permitted.

Although the Applicants do not agree with the Examiner, in the interest of expediting prosecution, claim 1 has been clarified to recite a non-naturally occurring intein or cleavage or cleavage and splicing moiety having splicing activity and/or controllable cleavage activity, wherein the intein is a truncated Mtu intein with the endonuclease domain deleted, and V67L and/or D422G mutation(s), wherein the truncated Mtu intein is ΔI-CM or ΔI-SM, or any full-length intein having a V67L and/or a D422G mutation(s). Therefore, the genus of inteins is the truncated Mtu intein ΔI-CM, the truncated Mtu intein ΔI-SM, a full-length intein having a V67L mutation, a full-length intein having a D422G mutation, and a full-length intein having both V67L and D422G mutations.

Applicants submitted concurrently as Exhibits 1-4 to demonstrate that one of ordinary skill in the art can make the inteins of the present invention by combining the teachings of the specification with what was known to one of ordinary skill in the art at the effective filing date. Specifically, Applicants demonstrate that one of ordinary skill in the art can take the teachings of the specification and apply it to what was known in the art to make the inteins of the present invention.

The amino acid sequence of the Applicants cite Davis et al. (Cell. 1992 Oct 16;71(2):201-10 submitted as reference AQ in the Information Disclosure Statement filed April 19, 2001) as a reference for the active, full-length Mtu *recA* intein (page 35, lines 30-31 of the specification). The Medline abstract of the Davis reference is attached hereto as Exhibit 1. In the upper-right hand corner of the Medline abstract is a hyperlink for "Links". Clicking the "Links" hyperlink reveals a submenu of hyperlinks and "Protein" is one of the hyperlinks. Upon clicking the "Protein" hyperlink, two Entrez Protein database submissions for the RecA protein P26345 and S18206 are revealed, attached hereto as Exhibit 2. The entry for Entrez Protein accession number P26345 is attached hereto as Exhibit 3. On the fifth page, line 22 of Exhibit 3, there is a hyperlink labeled "Region" that corresponds to the mature chain of the Endonuclease PI-MtuI. Upon clicking of the above-mentioned "Region" hyperlink, an entry for the Endonuclease PI-MtuI (Mtu recA intein) is revealed and attached hereto as Exhibit 4. The full-length sequence of

the Mtu *recA* intein is on the sixth page of Exhibit 4. The valine (V) at position 67 and the aspartic acid (D) at position 422 are indicated by double underlining.

The characteristics of ΔI-CM or ΔI-SM are described in the specification as originally filed (see, e.g., page 12, line 28, page 13, line 1, page 17, line 29, page 24, lines 5-9, page 26, lines 28-30, page 36, lines 7-9 and 23-26 and Figure 2). The sequence of the ΔI-CM or ΔI-SM inteins can be constructed with the amino acid sequence of full-length Mtu *recA* intein when combined with the teachings of the specification. The ΔI intein is described as the first 110 and the last 58 amino acids of the Mtu *recA* intein (see, e.g., page 36, lines 2-3 and Derbyshire et al., Proc Natl Acad Sci U S A. 1997 Oct 14;94(21):11466-71 submitted as reference CS in an Information Disclosure statement filed April 19, 2001). The mutations identified in ΔI-CM and ΔI-SM are also described (see, e.g., page 36, lines 9 and 24-26). Therefore, Applicants submit that the description in the specification suffices for one of skill in the art to make and use the truncated Mtu inteins ΔI-CM or ΔI-SM.

Applicants also submit that the description in the specification for full-length Mtu *recA* inteins having a V67L and/or a D422G mutation(s) is sufficient for one of ordinary skill in the art to make the full-length mutein inteins without undue experimentation. Applicants identified novel mutations V67L and D422G that affect intein splicing activity and/or controllable cleavage activity. The amino acid sequence of the full-length Mtu *recA* intein was known to one of ordinary skill in the art (as discussed *supra*). Thus, a full-length Mtu *recA* intein having a V67L and/or a D422G mutation(s)can be constructed by one of ordinary skill in the art without undue experimentation.

It is believed that the rejections under 35 U.S.C. § 112, first paragraph, have been overcome. Reconsideration and withdrawal are requested.

5.   The Rejections Under 35 U.S.C. § 102(e) Are Overcome

Claims 1-8, 11-14 and 16-33 were rejected under 35 U.S.C. §102(e) as allegedly anticipated by Comb *et al.* (U.S. Patent No. 5,834,247, hereinafter "Comb"). This rejection is respectfully traversed. This rejection is moot in light of the amendments to the claims submitted herein. The cited reference does not anticipate the instant invention.

The Examiner alleges that the molecule disclosed by Comb is a non-naturally occurring intein which is "very similar" to a Mtu intein with the endonuclease domain deleted, and V67L

and/or D422G mutation or any intein having a D to G mutation in a location corresponding to residue 422 of the full-length Mtu intein.

The instant invention relates to a non-naturally occurring intein or cleavage or cleavage and splicing moiety having splicing activity and/or controllable cleavage activity, wherein the intein is a truncated Mtu intein with the endonuclease domain deleted, and V67L and/or D422G mutation(s), wherein the truncated Mtu intein is ΔI-CM or ΔI-SM, or any full-length intein having a V67L and/or a D422G mutation(s). The intein of the present invention is not disclosed, suggested or enabled by Comb.

It is respectfully pointed out that a two-prong inquiry must be satisfied in order for a Section 102 rejection to stand. First, the prior art reference must contain all of the elements of the claimed invention. *See Lewmar Marine Inc. v. Barient Inc.,* 3 U.S.P.Q.2d 1766 (Fed. Cir. 1987). Second, the prior art must contain an enabling disclosure. *See Chester v. Miller,* 15 U.S.P.Q.2d 1333, 1336 (Fed. Cir. 1990). A reference contains an enabling disclosure if a person of ordinary skill in the art could have combined the description of the invention in the prior art reference with his own knowledge of the art to have placed himself in possession of the invention. *See In re Donohue,* 226, U.S.P.Q. 619, 621 (Fed. Cir. 1985).

Applying the law to the instant facts, the reference relied upon by the Office Action does not disclose, suggest or enable Applicants' invention. Comb does not teach, suggest or enable a non-naturally occurring intein or cleavage or cleavage and splicing moiety having splicing activity and/or controllable cleavage activity, wherein the intein is a truncated Mtu intein with the endonuclease domain deleted, and V67L and/or D422G mutation(s), wherein the truncated Mtu intein is ΔI-CM or ΔI-SM, or any full-length intein having a V67L and/or a D422G mutation(s). These mutations enable rapid cleaving in this intein and gives them superior capabilities to the inteins of Combs.

Comb does not teach, suggest or enable any D (aspartic acid) to G (glycine) or V (valine) to L (leucine) mutations. The only substitution mutations that Comb illustrates are (1) a single amino acid change at the serine 1082 of CIVPS2 (col. 11, line 31-33), (2) amino acid substitutions for the threonine 1472 residue of CIVPS2 (col. 11, lines 49-53), (3) an arginine substitution at position 1079 of CIVPS2 (col. 12, lines 40-43), and (4) an alanine substitution for the aspartate 1236 residue (col. 13, lines 54-57). Thus, Comb does not contain all of the elements of the presently claimed invention.

Consequently, reconsideration and withdrawal of the Section 102 rejections are earnestly requested.

00190034

REQUEST FOR INTERVIEW

If any issue remains as an impediment to allowance, a further interview with the Examiner and SPE are respectfully requested; and, the Examiner is additionally requested to contact the undersigned to arrange a mutually convenient time and manner for such an interview.

CONCLUSION

In view of the remarks and amendments herewith, the application is believed to be in condition for allowance. Favorable reconsideration of the application and prompt issuance of a Notice of Allowance are earnestly solicited. The undersigned looks forward to hearing favorably from the Examiner at an early date, and, the Examiner is invited to telephonically contact the undersigned to advance prosecution. The Commission is authorized to charge any fee occasioned by this paper, or credit any overpayment of such fees, to Deposit Account No. 50-0320.

Respectfully submitted,
FROMMER LAWRENCE & HAUG LLP

By: *Deborah d. du*

Thomas J. Kowalski
Reg. No. 32,147
Deborah L. Lu
Reg. No. 50,940
Telephone: (212) 588-0800
Facsimile: (212) 588-0500

EXHIBIT 1

Protein splicing in the maturation of M. tuberculosis recA protein: a mechanism for tolerating a novel class of intervening sequence.

Davis EO, Jenner PJ, Brooks PC, Colston MJ, Sedgwick SG.

Laboratory for Leprosy and Mycobacterial Research, National Institute for Medical Research, Mill Hill, London, England.

The M. tuberculosis recA locus comprises an 85 kd open reading frame but produced 38 kd RecA and 47 kd products in E. coli. No RNA processing was detected; rather, an 85 kd precursor protein was spliced, releasing a 47 kd spacer protein, and joining its terminal fragments to form mature RecA protein. "Spacer" protein was also produced in M. tuberculosis and from a hybrid spacer-LacZ alpha fusion molecule. Mutagenesis at codon wobble positions at one splice junction showed that protein rather than nucleotide sequence determined splicing activity. Other mutants defined additional regions needed for splicing and allowed processing to be followed. Splicing was essential for RecA activity in E. coli. The possibility that splicing is a manifestation of a novel class of genetic element is discussed.

EXHIBIT 2

1: P26345

RecA protein (Recombinase A) [Contains: Endonuclease PI-MtuI (Mtu recA intein)]
gi|132229|sp|P26345|RECA_MYCTU[132229]

2: S18206

recombination protein recA precursor - Mycobacterium tuberculosis (strain H37RV)
gi|98821|pir||S18206[98821]

00190034

EXHIBIT 3

LOCUS   P26345   790 aa   linear BCT 15-MAR-2004

DEFINITION RecA protein (Recombinase A) [Contains: Endonuclease PI-Mtul (Mtu

recA intein)].

ACCESSION P26345

VERSION   P26345 GI:132229

DBSOURCE swissprot: locus RECA_MYCTU, accession P26345;

class: standard.

extra accessions:O34519,created: May 1, 1992.

sequence updated: May 1, 1992.

annotation updated: Mar 15, 2004.

xrefs: gi: 44661, gi: 44662, gi: 2597999, gi: 2598000, gi: 2598001,

gi: 2598002, gi: 41353422, gi: 2624258, gi: 13882564, gi: 13882569,

gi: 31619300, gi: 31619503, gi: 98821, pdb accession 1G18, pdb

accession 1G19, pdb accession 1MO3, pdb accession 1MO4, pdb

accession 1MO5, pdb accession 1MO6

xrefs (non-sequence databases): REBASE2629, TIGRMT2806,

TubercuListRv2737c, HAMAPMF_00268, InterProIPR003593,

InterProIPR003587, InterProIPR003586, InterProIPR006142,

InterProIPR004042, InterProIPR006141, InterProIPR001553,

PfamPF00154, PRINTSPR00379, PRINTSPR00142, ProDomPD000229,

SMARTSM00382, SMARTSM00305, SMARTSM00306, TIGRFAMsTIGR01443,

TIGRFAMsTIGR01445, PROSITEPS50818, PROSITEPS50819, PROSITEPS50817,

PROSITEPS00321, PROSITEPS50162, PROSITEPS50163

KEYWORDS   DNA damage; DNA recombination; SOS response; ATP-binding;

DNA-binding; Autocatalytic cleavage; Protein splicing; Hydrolase;

Nuclease; Endonuclease; Intron homing; Complete proteome;

3D-structure.

SOURCE   Mycobacterium tuberculosis

ORGANISM Mycobacterium tuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

tuberculosis complex.

REFERENCE 1 (residues 1 to 790)

AUTHORS Davis,E.O., Sedgwick,S.G. and Colston,M.J.

TITLE   Novel structure of the recA locus of Mycobacterium tuberculosis

implies processing of the gene product

JOURNAL J. Bacteriol. 173 (18), 5653-5662 (1991)

MEDLINE 91358354

PUBMED 1909321

REMARK SEQUENCE FROM N.A.

SPECIES=M.tuberculosis; STRAIN=H37Rv

REFERENCE 2 (residues 1 to 790)

AUTHORS Vansoolingen,D., Hoogenboezem,T., Dehaas,P.E. and Hermans,P.W.M.

TITLE Direct Submission

JOURNAL Submitted (~JUL-1997)

REMARK SEQUENCE FROM N.A.

SPECIES=M.tuberculosis; STRAIN=Canetti, and SO93

REFERENCE 3 (residues 1 to 790)

AUTHORS Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,

Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry,C.E. III,

Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,

Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,

Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,

Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,

Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,

Squares,S., Squares,R., Sulston,J.E., Taylor,K., Whitehead,S. and

Barrell,B.G.

TITLE Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence

JOURNAL Nature 393 (6685), 537-544 (1998)

MEDLINE 98295987

PUBMED 9634230

REMARK SEQUENCE FROM N.A.

SPECIES=M.tuberculosis; STRAIN=H37Rv

REFERENCE 4 (residues 1 to 790)

AUTHORS Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,

Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D.H., Hickey,E.,

Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,

Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,

Gill,J., Mikula,A., Bishai,W., Jacobs,W.R.Jr., Venter,J.C. and

Fraser,C.M.

TITLE Whole-genome comparison of Mycobacterium tuberculosis clinical and

laboratory strains

JOURNAL J. Bacteriol. 184 (19), 5479-5490 (2002)

MEDLINE 22206494

PUBMED 12218036

REMARK SEQUENCE FROM N.A.

SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh

REFERENCE 5 (residues 1 to 790)

AUTHORS Garnier,T., Eiglmeier,K., Camus,J.-C., Medina,N., Mansoor,H.,
Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S.,
Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L.,
Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and
Hewinson,R.G.

TITLE The complete genome sequence of Mycobacterium bovis

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7877-7882 (2003)

MEDLINE 22709107

PUBMED 12788972

REMARK SEQUENCE FROM N.A.

SPECIES=M.bovis; STRAIN=AF2122/97

REFERENCE 6 (residues 1 to 790)

AUTHORS Davis,E.O., Jenner,P.J., Brooks,P.C., Colston,M.J. and
Sedgwick,S.G.

TITLE Protein splicing in the maturation of M. tuberculosis recA protein:
a mechanism for tolerating a novel class of intervening sequence

JOURNAL Cell 71 (2), 201-210 (1992)

MEDLINE 93046621

PUBMED 1423588

REMARK PROTEIN SPLICING.

SPECIES=M.tuberculosis

REFERENCE 7 (residues 1 to 790)

AUTHORS Kumar,R.A., Vaze,M.B., Chandra,N.R., Vijayan,M. and Muniyappa,K.

TITLE Functional characterization of the precursor and spliced forms of
RecA protein of Mycobacterium tuberculosis

JOURNAL Biochemistry 35 (6), 1793-1802 (1996)

MEDLINE 96229901

PUBMED 8639660

REMARK CHARACTERIZATION.

SPECIES=M.tuberculosis

REFERENCE 8 (residues 1 to 790)

AUTHORS Colston,M.J. and Davis,E.O.

JOURNAL   (in) Bloom,B.R. (Ed.);

TUBERCULOSIS: PATHOGENESIS, PROTECTION AND CONTROL: 217-226;

American Society for Microbiology, Washington D.C. (1994)

REMARK   REVIEW.

SPECIES=M.tuberculosis

REFERENCE   9   (residues 1 to 790)

AUTHORS   Datta,S., Prabu,M.M., Vaze,M.B., Ganesh,N., Chandra,N.R.,

Muniyappa,K. and Vijayan,M.

TITLE   Crystal structures of Mycobacterium tuberculosis RecA and its

complex with ADP-AIF(4): implications for decreased ATPase activity

and molecular aggregation

JOURNAL   Nucleic Acids Res. 28 (24), 4964-4973 (2000)

MEDLINE   20572535

PUBMED   11121488

REMARK   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).

SPECIES=M.tuberculosis

COMMENT   --

This SWISS-PROT entry is copyright. It is produced through a

collaboration between the Swiss Institute of Bioinformatics and

the EMBL outstation - the European Bioinformatics Institute.

The original entry is available from http://www.expasy.ch/sprot

and http://www.ebi.ac.uk/sprot

--.

[FUNCTION] Can catalyze the hydrolysis of ATP in the presence of

single-stranded DNA, the ATP-dependent uptake of single-stranded

DNA by duplex DNA, and the ATP-dependent hybridization of

homologous single-stranded DNAs. It interacts with lexA causing its

activation and leading to its autocatalytic cleavage.

[FUNCTION] PI-Mtul is an endonuclease.

[SUBCELLULAR LOCATION] Cytoplasmic (By similarity).

[PTM] This protein undergoes a protein self splicing that involves

a post-translational excision of the intervening region (intein)

followed by peptide ligation.

[SIMILARITY] Belongs to the recA family.

[SIMILARITY] In the intein section; belongs to the homing

endonuclease family.

FEATURES   Location/Qualifiers

source   1..790

/organism="Mycobacterium bovis"

/db_xref="taxon:1765"

source   1..790

/organism="Mycobacterium tuberculosis"

/db_xref="taxon:1773"

gene   1..790

/gene="RECA"

/note="synonyms: RV2737C, MT2806, MTV002.02C, MB2756C"

Protein   1..790

/gene="RECA"

/product="RecA protein"

/EC_number="3.1.-.-"

Region   1..251

/gene="RECA"

/region_name="Mature chain"

/note="RecA protein, 1st part."

Site   67..74

/gene="RECA"

/site_type="np-binding"

/note="ATP (By similarity)."

Region   252..691

/gene="RECA"

/region_name="Mature chain"

/note="Endonuclease PI-Mtul."

Region   305

/gene="RECA"

/region_name="Variant"

/note="R -> Q (IN STRAINS CANETTI AND SO93)."

Region   430

/gene="RECA"

/region_name="Variant"

/note="A -> L (IN STRAINS CANETTI AND SO93)."

Region   434..435

/gene="RECA"

/region_name="Variant"

/note="QQ -> RR (IN STRAINS CANETTI AND SO93)."

00190034

Region   438..439

/gene="RECA"

/region_name="Variant"

/note="IY -> VH (IN STRAINS CANETTI AND SO93)."

Region   692..790

/gene="RECA"

/region_name="Mature chain"

/note="RecA protein, 2nd part."

ORIGIN

```
  1 mtqtpdreka lelavaqiek sygkgsvmrl gdearqpisv iptgsialdv algigglprg
 61 rvieiygpes sgkttvalha vanaqaaggv aafidaehal dpdyakklgv dtdsllvsqp
121 dtgeqaleia dmlirsgald ivvidsvaal vpraelegem gdshvglqar lmsqalrkmt
181 galnnsgtta ifinqlrdki gvmfgspett tggkalkfya svrmdvrrve tlkdgtnavg
241 nrtrvkvvkn kclaegtrif dpvtgtthri edvvdgrkpi hvvaaakdgt lharpvvswf
301 dqgtrdvigl riaggaivwa tpdhkvltey gwraagelrk gdrvaqprrf dgfgdsapip
361 adharllgyl igdgrdgwvg gktpinfinv qraliddvtr iaatlgcaah pqgrislaia
421 hrpgerngva dlcqqagiyg klawektipn wffepdiaad ivgnllfglf esdgwvsreq
481 tgalrvgytt tseqlahqih wlllrfgvgs tvrdydptqk rpsivngrri qskrqvfevr
541 isgmdnvtaf aesvpmwgpr gaaliqaipe atqgrrrgsq atylaaemtd avlnylderg
601 vtaqeaaami gvasgdprgg mkqvlgasrl rrdrvqalad alddkflhdm laeelrysvi
661 revlptrrar tfdleveelh tlvaegvvvh ncsppfkqae fdilygkgis regslidmgv
721 dqglirksga wftyegeqlg qgkenarnfl venadvadei ekkikeklgi gavvtddpsn
781 dgvlpapvdf
```

//

EXHIBIT 4

LOCUS   P26345   440 aa   linear BCT 15-MAR-2004

DEFINITION RecA protein (Recombinase A) [Contains: Endonuclease PI-Mtul (Mtu recA intein)].

ACCESSION   P26345 REGION: 252..691

VERSION   P26345 GI:132229

DBSOURCE   swissprot: locus RECA_MYCTU, accession P26345;

class: standard.

extra accessions:O34519,created: May 1, 1992.

sequence updated: May 1, 1992.

annotation updated: Mar 15, 2004.

xrefs: gi: 44661, gi: 44662, gi: 2597999, gi: 2598000, gi: 2598001,

gi: 2598002, gi: 41353422, gi: 2624258, gi: 13882564, gi: 13882569,

gi: 31619300, gi: 31619503, gi: 98821, pdb accession 1G18, pdb

accession 1G19, pdb accession 1MO3, pdb accession 1MO4, pdb

accession 1MO5, pdb accession 1MO6

xrefs (non-sequence databases): REBASE2629, TIGRMT2806,

TubercuListRv2737c, HAMAPMF_00268, InterProIPR003593,

InterProIPR003587, InterProIPR003586, InterProIPR006142,

InterProIPR004042, InterProIPR006141, InterProIPR001553,

PfamPF00154, PRINTSPR00379, PRINTSPR00142, ProDomPD000229,

SMARTSM00382, SMARTSM00305, SMARTSM00306, TIGRFAMsTIGR01443,

TIGRFAMsTIGR01445, PROSITEPS50818, PROSITEPS50819, PROSITEPS50817,

PROSITEPS00321, PROSITEPS50162, PROSITEPS50163

KEYWORDS   DNA damage; DNA recombination; SOS response; ATP-binding;

DNA-binding; Autocatalytic cleavage; Protein splicing; Hydrolase;

Nuclease; Endonuclease; Intron homing; Complete proteome;

3D-structure.

SOURCE   Mycobacterium tuberculosis

 ORGANISM Mycobacterium tuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium

tuberculosis complex.

REFERENCE 1 (residues 1 to 440)

 AUTHORS   Davis,E.O., Sedgwick,S.G. and Colston,M.J.

 TITLE   Novel structure of the recA locus of Mycobacterium tuberculosis

implies processing of the gene product

 JOURNAL J. Bacteriol. 173 (18), 5653-5662 (1991)

MEDLINE   91358354

 PUBMED   1909321

REMARK   SEQUENCE FROM N.A.

        SPECIES=M.tuberculosis; STRAIN=H37Rv

REFERENCE   2 (residues 1 to 440)

AUTHORS   Vansoolingen,D., Hoogenboezem,T., Dehaas,P.E. and Hermans,P.W.M.

TITLE   Direct Submission

JOURNAL   Submitted (~JUL-1997)

REMARK   SEQUENCE FROM N.A.

        SPECIES=M.tuberculosis; STRAIN=Canetti, and SO93

REFERENCE   3 (residues 1 to 440)

AUTHORS   Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,

        Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry,C.E. III,

        Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,

        Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,

        Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,

        Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,

        Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,

        Squares,S., Squares,R., Sulston,J.E., Taylor,K., Whitehead,S. and

        Barrell,B.G.

TITLE   Deciphering the biology of Mycobacterium tuberculosis from the

        complete genome sequence

JOURNAL   Nature 393 (6685), 537-544 (1998)

MEDLINE   98295987

 PUBMED   9634230

REMARK   SEQUENCE FROM N.A.

        SPECIES=M.tuberculosis; STRAIN=H37Rv

REFERENCE   4 (residues 1 to 440)

AUTHORS   Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,

        Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D.H., Hickey,E.,

        Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,

        Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,

        Gill,J., Mikula,A., Bishai,W., Jacobs,W.R.Jr., Venter,J.C. and

        Fraser,C.M.

TITLE   Whole-genome comparison of Mycobacterium tuberculosis clinical and

        laboratory strains

JOURNAL   J. Bacteriol. 184 (19), 5479-5490 (2002)

MEDLINE   22206494

PUBMED   12218036

REMARK   SEQUENCE FROM N.A.

SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh

REFERENCE   5 (residues 1 to 440)

AUTHORS   Garnier,T., Eiglmeier,K., Camus,J.-C., Medina,N., Mansoor,H.,

Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S.,

Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L.,

Wheeler,P.R., Parkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and

Hewinson,R.G.

TITLE   The complete genome sequence of Mycobacterium bovis

JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7877-7882 (2003)

MEDLINE   22709107

PUBMED   12788972

REMARK   SEQUENCE FROM N.A.

SPECIES=M.bovis; STRAIN=AF2122/97

REFERENCE   6 (residues 1 to 440)

AUTHORS   Davis,E.O., Jenner,P.J., Brooks,P.C., Colston,M.J. and

Sedgwick,S.G.

TITLE   Protein splicing in the maturation of M. tuberculosis recA protein:

a mechanism for tolerating a novel class of intervening sequence

JOURNAL   Cell 71 (2), 201-210 (1992)

MEDLINE   93046621

PUBMED   1423588

REMARK   PROTEIN SPLICING.

SPECIES=M.tuberculosis

REFERENCE   7 (residues 1 to 440)

AUTHORS   Kumar,R.A., Vaze,M.B., Chandra,N.R., Vijayan,M. and Muniyappa,K.

TITLE   Functional characterization of the precursor and spliced forms of

RecA protein of Mycobacterium tuberculosis

JOURNAL   Biochemistry 35 (6), 1793-1802 (1996)

MEDLINE   96229901

PUBMED   8639660

REMARK   CHARACTERIZATION.

SPECIES=M.tuberculosis

REFERENCE   8 (residues 1 to 440)

AUTHORS   Colston,M.J. and Davis,E.O.

JOURNAL   (in) Bloom,B.R. (Ed.);

TUBERCULOSIS: PATHOGENESIS, PROTECTION AND CONTROL: 217-226;

American Society for Microbiology, Washington D.C. (1994)

REMARK   REVIEW.

SPECIES=M.tuberculosis

REFERENCE 9 (residues 1 to 440)

 AUTHORS   Datta,S., Prabu,M.M., Vaze,M.B., Ganesh,N., Chandra,N.R.,

Muniyappa,K. and Vijayan,M.

 TITLE   Crystal structures of Mycobacterium tuberculosis RecA and its

complex with ADP-AlF(4): implications for decreased ATPase activity

and molecular aggregation

JOURNAL   Nucleic Acids Res. 28 (24), 4964-4973 (2000)

MEDLINE   20572535

 PUBMED   11121488

REMARK   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).

SPECIES=M.tuberculosis

COMMENT   ---

This SWISS-PROT entry is copyright. It is produced through a

collaboration between the Swiss Institute of Bioinformatics and

the EMBL outstation - the European Bioinformatics Institute.

The original entry is available from http://www.expasy.ch/sprot

and http://www.ebi.ac.uk/sprot

---.

[FUNCTION] Can catalyze the hydrolysis of ATP in the presence of

single-stranded DNA, the ATP-dependent uptake of single-stranded

DNA by duplex DNA, and the ATP-dependent hybridization of

homologous single-stranded DNAs. It interacts with lexA causing its

activation and leading to its autocatalytic cleavage.

[FUNCTION] PI-MtuI is an endonuclease.

[SUBCELLULAR LOCATION] Cytoplasmic (By similarity).

[PTM] This protein undergoes a protein self splicing that involves

a post-translational excision of the intervening region (intein)

followed by peptide ligation.

[SIMILARITY] Belongs to the recA family.

[SIMILARITY] In the intein section; belongs to the homing

endonuclease family.

FEATURES   Location/Qualifiers

source   1..440

/organism="Mycobacterium bovis"

/db_xref="taxon:1765"

source   1..440

/organism="Mycobacterium tuberculosis"

/db_xref="taxon:1773"

gene   <1..>440

/gene="RECA"

/note="synonyms: RV2737C, MT2806, MTV002.02C, MB2756C"

Protein   <1..>440

/gene="RECA"

/product="RecA protein"

/EC_number="3.1.-.-"

Region   1..440

/gene="RECA"

/region_name="Mature chain"

/note="Endonuclease PI-MtuI."

Region   54

/gene="RECA"

/region_name="Variant"

/note="R -> Q (IN STRAINS CANETTI AND SO93)."

Region   179

/gene="RECA"

/region_name="Variant"

/note="A -> L (IN STRAINS CANETTI AND SO93)."

Region   183..184

/gene="RECA"

/region_name="Variant"

/note="QQ -> RR (IN STRAINS CANETTI AND SO93)."

Region   187..188

/gene="RECA"

/region_name="Variant"

/note="IY -> VH (IN STRAINS CANETTI AND SO93)."

ORIGIN

```
  1 claegtrifd pvtgtthrie dvvdgrkpih vvaaakdgtl harpvvswfd qgtrdviglr
 61 iaggaivwat pdhkvlteyg wraagelrkg drvaqprrfd gfgdsapipa dharllgyli
121 gdgrdgwvgg ktpinfinvq raliddvtri aatlgcaahp qgrislaiah rpgerngvad
181 lcqqagiygk lawektipnw ffepdiaadi vgnllfglfe sdgwvsreqt galrvgyttt
241 seqlahqihw lllrfgvgst vrdydptqkr psivngrriq skrqvfevri sgmdnvtafa
301 esvpmwgprg aaliqaipea tqgrrrgsqa tylaaemtda vlnyldergv taqeaaamig
361 vasgdprggm kqvlgasrlr rdrvqalada lddkflhdml aeelrysvir evlptrrart
421 fdleveelht lvaegvvvhn
```